

FIG.1

```

graph TD
    A[Prepar Master Cell Stock MCS] --> B[Prepare MCS+n]
    A --> C[Genetically Alter PRRS Virus]
    B --> C
    B --> D[Prepare Working Cell Stock]
    C --> E[Plaque-purify Genetically Altered Vaccine Virus 3 Times]
    E --> F[Prepare Master Seed Virus MSV(X), MSV(X+1), MSV(X+2) and MSV(X+3)]
    F --> G[Prepare Working Seed Virus MSV(X+4)]
    D --> H[Prepare Prototype Vaccine MSV(X+5)]
    G --> H
    H --> I[Perform Efficacy Studies]
    I --> J[Perform Safety Studies]
    J --> K[Submit Research Data to NVSL]
    K --> L[Obtain Vaccine License]
    I --> M[Develop Pig Challenge Models]
    I --> N[Develop Clinical Assays]
    I --> O[Develop Potency Assay]
  
```

FIGURE 2

ISU-12 cDNA λ Library Construction

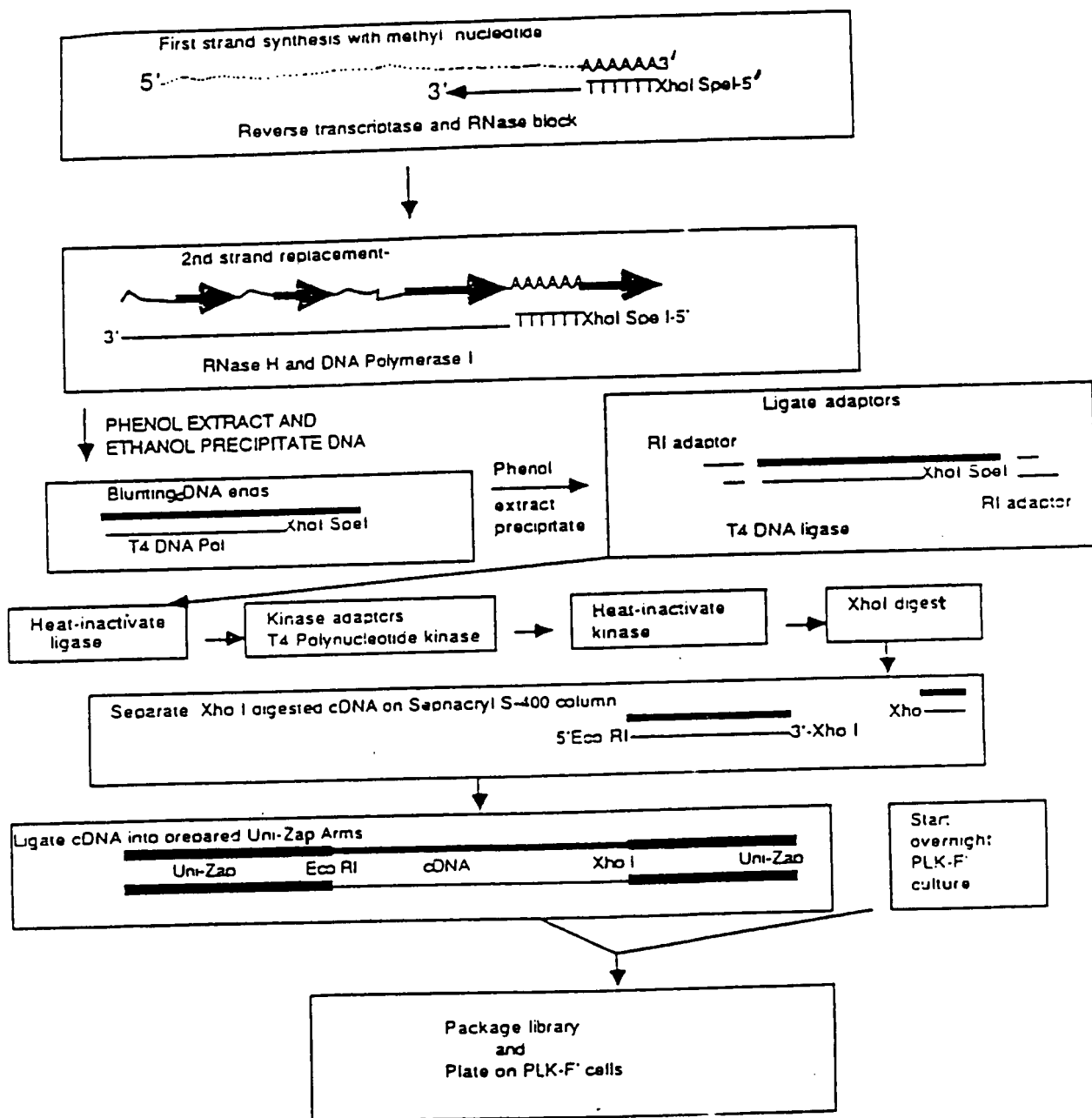


FIGURE 3

Identification of ISU-12 Authentic Clones by Differential Hybridization

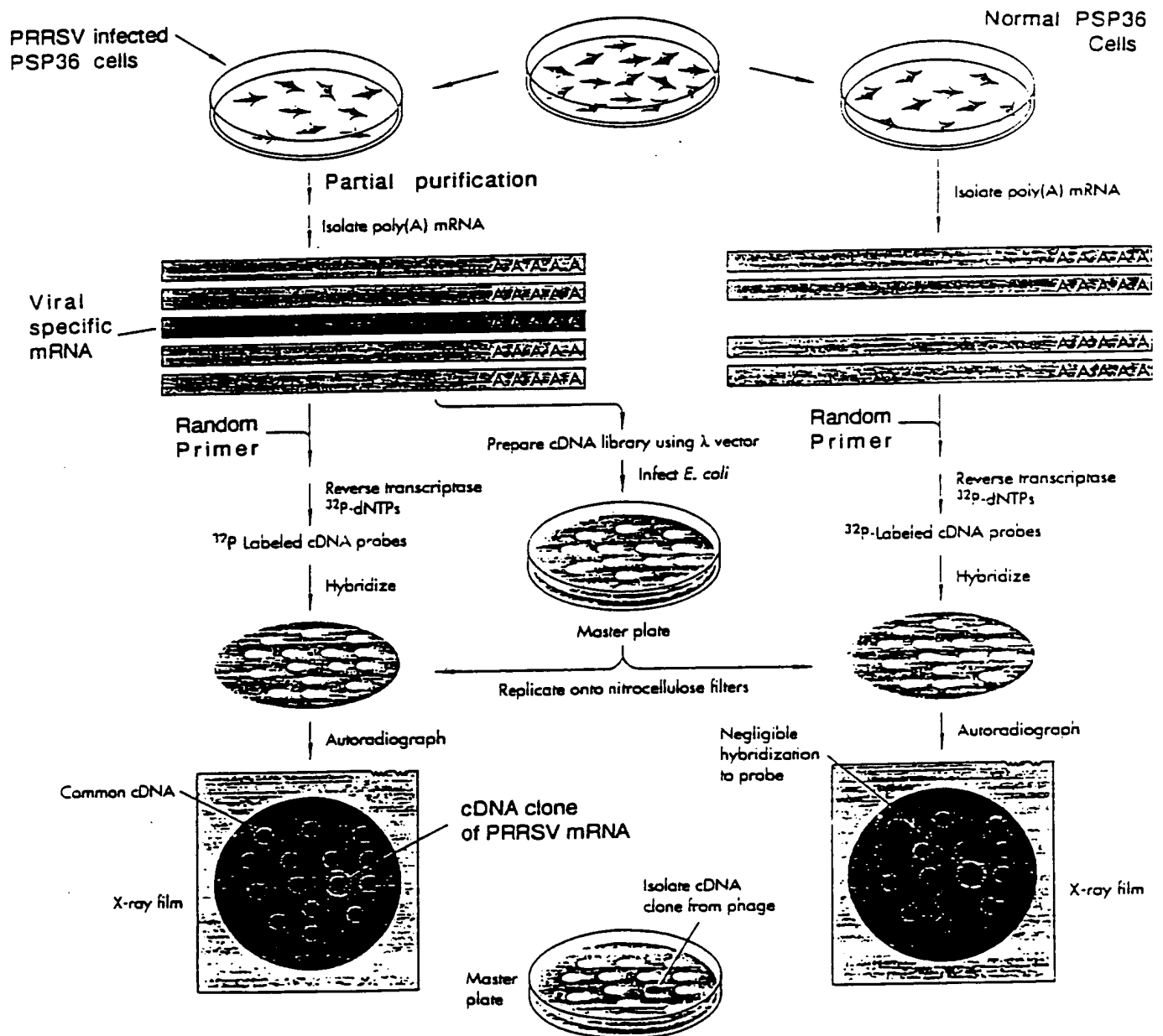


FIGURE 4

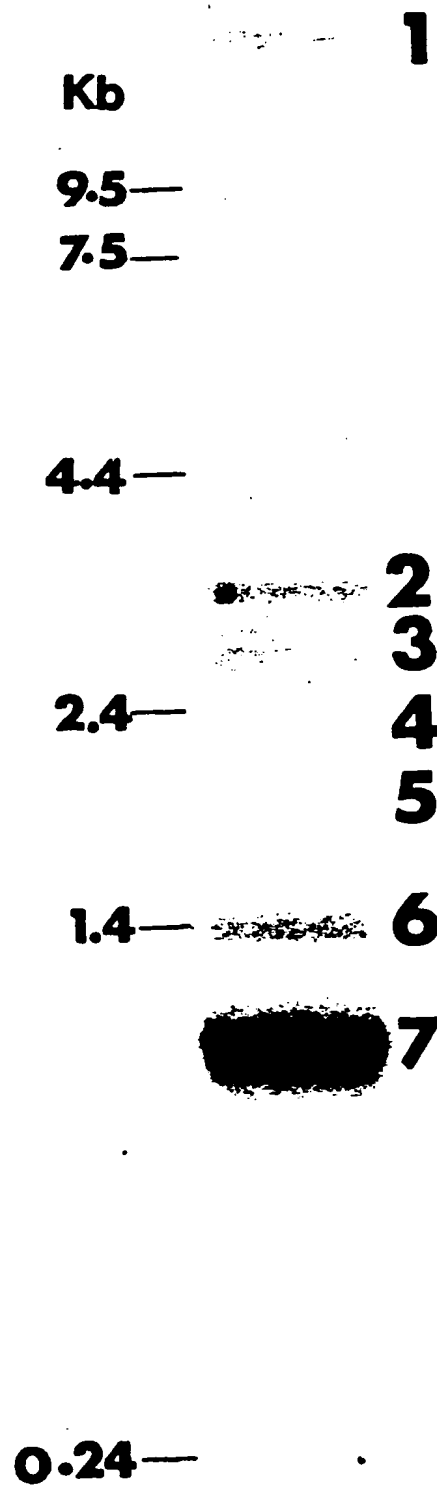


FIGURE 5

ISU-12-7a 3' terminal Graphics

FIGURE 6

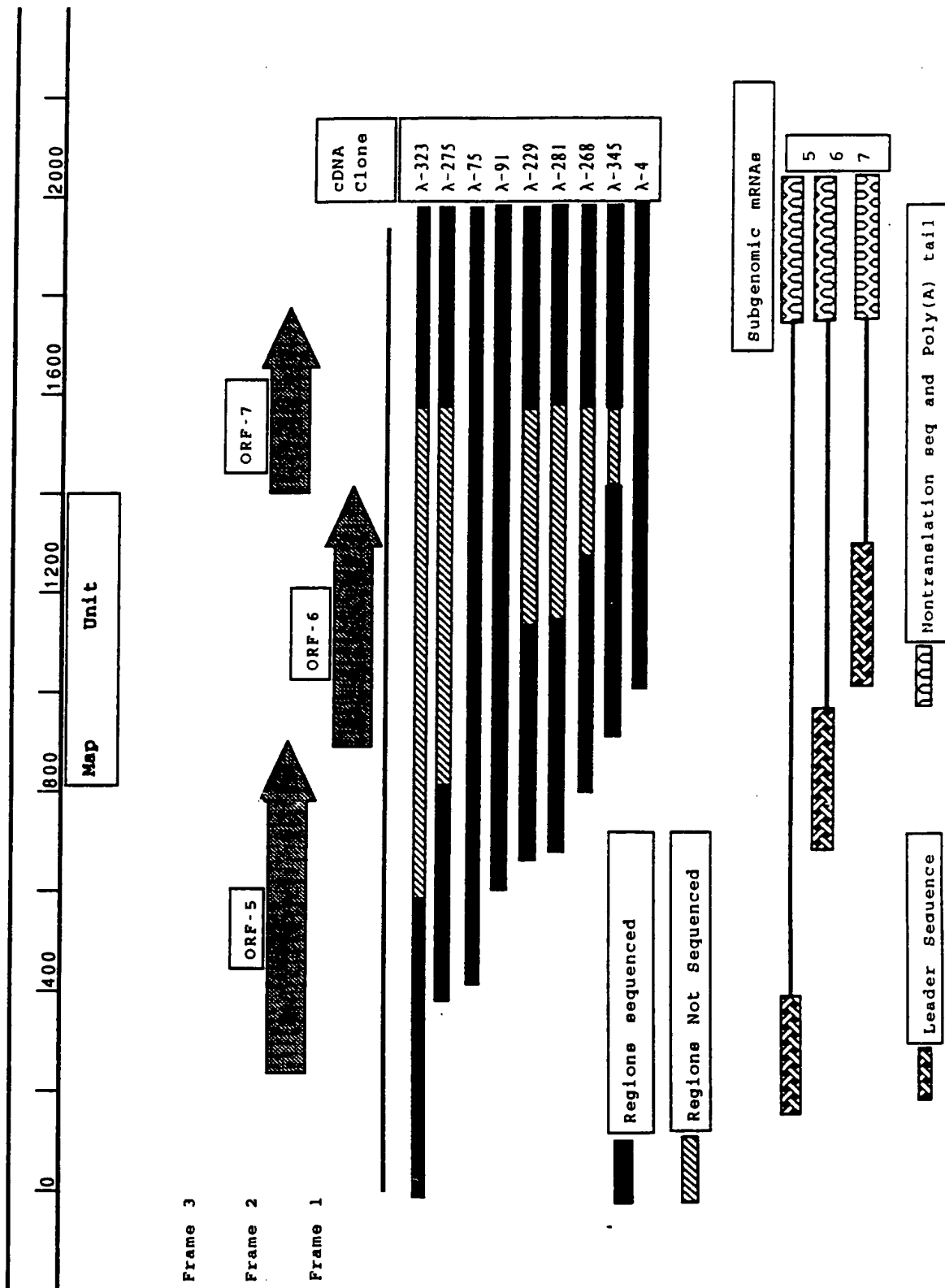


FIGURE 7

GGCAGGCTTTGCTGTCTCCCAAGACATCAGTTGCCCTTAGGCATCGCAACTCGGCCTCTGAGGCGATTTCGCAAAGTCCCTCAGTGC CGCACGGCGATAGGG 100

ACACCCGCTGTATATCACTGTTCACAGCCAATGTTACCGATGAGAAATTATTTGCAATTCCTCTGATCTTCTCATGCTTTCTTCTGCTTTTCTATGCTTCTG 200

AGATGAGTGAAAAAGGATTTAAGGTGGTATTTTGGCAATGTGTACGGCATCGTGGCAGTGTGCGTCAACTTCACCAGTTACGTCCAACATGTCAAGGAATT 300

TACCCAAAGCTTCTTGGTAGTTGACCATGTGCGGCTGCTCCATTTTCATGACGCCCCGAGACCATGAGGTGGGCAACTGCTTTTAGCTGTCTTTTGGCATT 400

CTGTGTGCAATT**TGA**ATGTTTAAGT**TATG**TTGGGAAATGCTTGACCGCGGCTGTGTCTCGCAATTGCTTTTPTGTGGTGTATCGTGCCGCTCTGTCTTT 500

*** **ORF4 stop** +1>**ORF5 start**

GTTGCGCTCGTACGCCCAACGGGAACAGCGGCTCAAATTTACAGCTGATTTTACAACCTTGACGCTATGTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600

AATTTGACTGGGCAGTGGAGTGTPTGTCAATTTTCTGTGTGACTCACATGTCTCTTATGGTGGCCCTCACTACTAGCCATTTCTTTGACACAGTCCG 700

TCTGGTCACTGTGTCTACCGCTGGGTTTGTTCACGGCGGTATGTTC TGAGTAGCATGTACGGGCTGTGTCCCTGGCTGCGTTGATTTGCTTCGTCATT 800

AGGC TTGCGAAGAAATGTCATGTCTGGCGCTACTCATGTACAGATA TACCAACTTTCTTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTCCGCTG 900

TCATCATAGAGAAAAAGGGCAAAGTTGAGGTGGAAGGTACCTGATCGACCTCAAAGAGTTGTGCTTGATGGTTCCGCGGCTACCCCTGTAAACCAGAGT 1000

TTTAGCGGAACA**ATG**GAGTGTCTCT**TAG**ATGACTTCTGTTCATGATAGCACGGCTCCACAAAAGGTGCTCTTGGCGTTTCTATTACCTACACGCCAGTGA 1100

*****ORF5 stop** +1>**ORF6 start**

TGATATATGCCCTAAAGGTGAGTGGCGGCGACTGCTAGGGCTTCTGCACCTTTTGGTCTTCTGTAATTGTGCTTTTACCTTCGGGTACATGACATTCGT 1200

CTACTTTTCAGAGTACAAATAAGSTGCGCTCACTATGAGAGCAGTAGTTTCACTCTCTTTGGGGGTGTACTCAGCCATAGAAACCTGGAAATTCATCACC 1300

TCCAGATGCCGCTTTGTCTTGTCTAGGCGCAAGTACATTTCTGGCCCCCTGCCACCAAGTTGAAAGTGC CGCAGGCTTTTCATCCGATTGCGGCAAATGATA 1400

ACCAGGCATTTTGTGCTCGGCGTCCCGGCTCCACTACGGTCAACGGCACATTTGGTGCCCGGTTAAAAAGCCTCGTGTGGGTGGCAGAAAAAGCTGTTAA 1500

ACAGGGAGTGGTAAACCTTTGTTAAAT**TAG**CCAAAT**TAA**CACCGGCAAGCAGCAGAGAAGAAAGAGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600

*****ORF6 stop** +1>**ORF7 start**

GC TGGTAAAGATCATCGCTCACCAAAACAGTCCAGAGGCAAGGGACCGGAAAGAAAAATAAGAAGAAAAACCGGAGAAGCCCCATTTCCCTCTAGCG 1700

ACTGAAGATGATGTACAGATCACCTTTACCCCTAGTGAGCGTCAATTGTGTCTGTCTGTCATCCAGACCGCTTTAATCAAGCGCTGGGACTTGCACCC 1800

TGTTCAGATTACGGGAGGATAAGTTACACTGTGGAGTTTAGTTTGCCTACGCATCATACTGTGCGCTGATCCGCGTCACAGCATCACCCCTAGCAT**TGA**TG 1900

*****ORF7 stop**

GGCTGGCATTTCTTGAAGCATCCAGTGTTTGAATTGGAAGATGCGTGGTGAATGGCACTGATTGACATTTGTGCTCTAAGTCACCTATTCAATTAGGGC 2000

GACCGTGTGGGGTAAGATTTAATTGGCGAGAACCACACGGCGAAATTAAAAAAAAAAAA 2062

ISU 12/7a/3' terminal (888 – 1413)	AATGGAGTGG TCCATTAGATG ACTTCGTGCA TCATAGGAGG GGTCCACAAA AGGTGCTCTTT	947
Lelystad seq (14077 – 14598)	-ATGG-GAGG -CCTAGAGG ATTITTCGAA CGATCCATATC GCCCCACAAA AGCTGGTGGT	14132
ISU 12/7a/3' terminal (888 – 1413)	GGCGTTTCTT ATTACCTACA GGGCAGTGAT GATATATGCC CTAAGGTGA GTCCGGGGCCG	1007
Lelystad seq (14077 – 14598)	AGCGTTTAGC ATCACATACA CACCTATTAAT GATATAGCCC CTTAAGGTGT CACGGGGCCG	14192
ISU 12/7a/3' terminal (888 – 1413)	ACTGCTTAGGG CTTCGCAAC TTTTGGTGT TCTGAATTTGT GCCTTCACT TCCGGTACAT	1067
Lelystad seq (14077 – 14598)	ACTCCCTGGG CTGTTCCACA TCCCTAATTAAT TCTGAAGTGT TCCCTTACAT TCGGATACAT	14252
ISU 12/7a/3' terminal (888 – 1413)	GACATTCGTG CACTTTCAGA GTACAAATAA GGTGGGCTC ACTATGGGAG CAGTAGTTGC	1127
Lelystad seq (14077 – 14598)	GACATATCTG CATTTTCAAT CCACCAACCG TGTGGGAC TTT ACCCTGGGGG CTGTTTG TGG-	14311
ISU 12/7a/3' terminal (888 – 1413)	ACTCTTTTGG GGGGTGTAAT CAGC-CATA GAAACCTGGA AATTCATCAC CTCCAGATGC	1185
Lelystad seq (14077 – 14598)	-CCCTTCTGT GGGGTGTTTA CAGCTTACACA GAGTCTAGGA AGTTTATCAC TTCCAGATGC	14370
ISU 12/7a/3' terminal (888 – 1413)	CGTTTGTGCT TGTACGCGG CAAGTACAT CTGGCCCCTG CCCAGCAGCT TGAAGTGGC	1245
Lelystad seq (14077 – 14598)	AGATTGTGTTT GCCTTGGCCG GCCATACAT CTGGCCCCTG CCCATCAGCT AGAAAGTGGT	14430
ISU 12/7a/3' terminal (888 – 1413)	GCAGCTTTTC ATCCGATTGC GCGAAATGAT AACCAAGCAT TTGTCTGCTGG GGTCCCGGC	1305
Lelystad seq (14077 – 14598)	GCAGGTCTCC ATTCAATCTC AGGCTCTGGT AACCGAGCAT AGCTGTGAG AAAGCCCGCA	14490
ISU 12/7a/3' terminal (888 – 1413)	TCCACTACGG TCAACGGCAC ATTGGTCCCG GGGTTAAAAA GCCTCGTGT TGGTGGCACA	1365
Lelystad seq (14077 – 14598)	CTAAGATCAG TGAACGGCAC TGTAGTACCA GCACITTCGGA GCCTCGTGCT GGGGGGCANA	14550
ISU 12/7a/3' terminal (888 – 1413)	AAGCTGTTA AACAGGAGT GGTAAACCTTT GTTAAATATG CCAAAATAA	1413
Lelystad seq (14077 – 14598)	CGACCTGTTA AAGGAGGAGT GGTAAACCTC GTCAAGTATG GCGCGTAA	14598

FIGURE 9

Lelystad seq (14588 – 14974)	ATGCCCGGTA AAAACCACTA- GCCAGAACAA AAAGAAAAGT A-CAG---C 14632
ISU 12/7a/3' terminal (1403 – 1774)	-----AT GCCAAATATAC ACCGGCAAGC AGCAGAAGAG 1434
Lelystad seq (14588 – 14974)	TCCGATGGGG AATGGCCAGC CAGTCAATCA ACTGTGCCAG TTGCTGGGTG 14681
ISU 12/7a/3' terminal (1403 – 1774)	AAAGAGGGGG GATGGCCAGC CAGTCAATCA GCTGTGCCAG ATTGCTGGG- 1483
Lelystad seq (14588 – 14974)	CAATGATATA GTCCAGGGC CAGCAACCTTA GGGG--A-GG ACAGGCCAATA 14728
ISU 12/7a/3' terminal (1403 – 1774)	-AA-GATCAT CCGTACCAA AACCACTCCA GAGGCACGG ACCGG---GA 1528
Lelystad seq (14588 – 14974)	AAGAAAAA-- ---G----- -CCTGAGAAG CCACATTTC CCGTGGGTGC 14766
ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAAATA AGAAGAAAAA CCGGAGAGAG CCGCATTTCC CTCACGGAG 1578
Lelystad seq (14588 – 14974)	TGAAGATGAC ATCGGCACC ACCTACCCA GACTGACGC TCCGTGTGCT 14816
ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAT GTCAGACATC AGTTTACCCC TAGTGAACCGT CAATTGTGTC 1628
Lelystad seq (14588 – 14974)	TGCAATCGAT CCAGACGGT TTCAATCAAG GCGGAGGAAG -TGGTGGCT 14865
ISU 12/7a/3' terminal (1403 – 1774)	TGTGTCAT CCAGACGGC TTTAATCAAG GCGGTGGAG TTGACG-C- 1677
Lelystad seq (14588 – 14974)	TTTATCCAGC GCGAAGGTCA GTTTACAGT TCAGTTTATG CTGCGGTG 14915
ISU 12/7a/3' terminal (1403 – 1774)	GTACAGATTCA GCGAGATTA GTTACACTG- GGAGTTTAGT TTCCCTACCC 1727
Lelystad seq (14588 – 14974)	CTCATACAGT GCGCCTGATTT GCGGTGAGTT CTACATCCGC CAGTCAGGT 14965
ISU 12/7a/3' terminal (1403 – 1774)	ATCATACTGT GCGCCTGATC CCGGTACAG CATCACCC-T CAG-CATCA- 1774
Lelystad seq (14588 – 14974)	GCAAGTTAA 14974
ISU 12/7a/3' terminal (1403 – 1774)	1774

FIGURE 10

ISU 12/7a/3' terminal (1775 – 1938)	TGGCGTGGCA TTCTTGAGGC ATCCAGTGT TTGAATTGGA	1814
Lelystad seq (14975 – 15101)	-----TT	14976
ISU 12/7a/3' terminal (1775 – 1938)	ACAATGGCTG GTGAATGGCA CTGATTGACA TTGTCCTCT	1854
Lelystad seq (14975 – 15101)	TGACAGTCAG CTGAATGGCC GCGATTGGCG TGTGCGCTCT	15016
ISU 12/7a/3' terminal (1775 – 1938)	AAGTCACCTA TTCAATTAGG GCGACGCTGT GCGGGTAACA	1800
Lelystad seq (14975 – 15101)	GAGTCACCTA TTCAATTAGG GCGATCACAT GCGGGTCATA	15056
ISU 12/7a/3' terminal (1775 – 1938)	TTTAAATT-GG GGAGAACCAC ACGGCCGAAA TTAAAAAAA	1933
Lelystad seq (14975 – 15101)	CTTAAATCAGG GAGGAACCAT GTGACCCAAA TTAAAAAAA	15096
ISU 12/7a/3' terminal (1775 – 1938)	AAAAA	1938
Lelystad seq (14975 – 15101)	AAAAA	15101

FIGURE 11

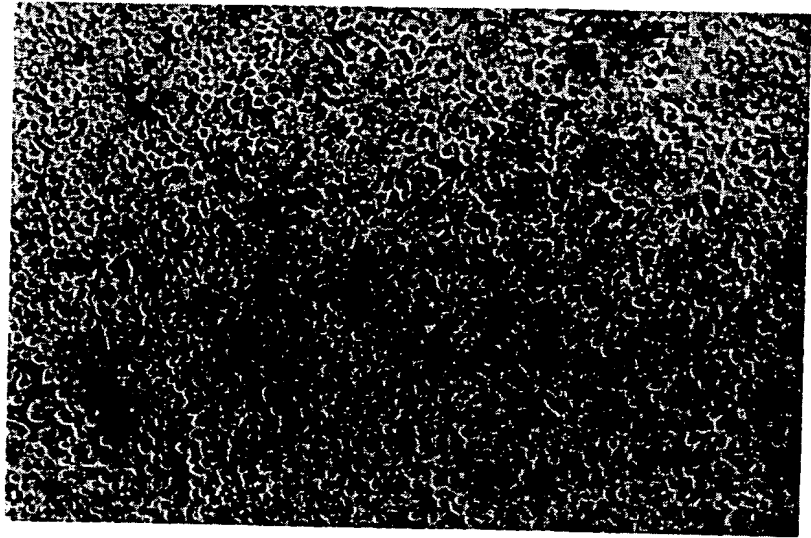


FIGURE 12

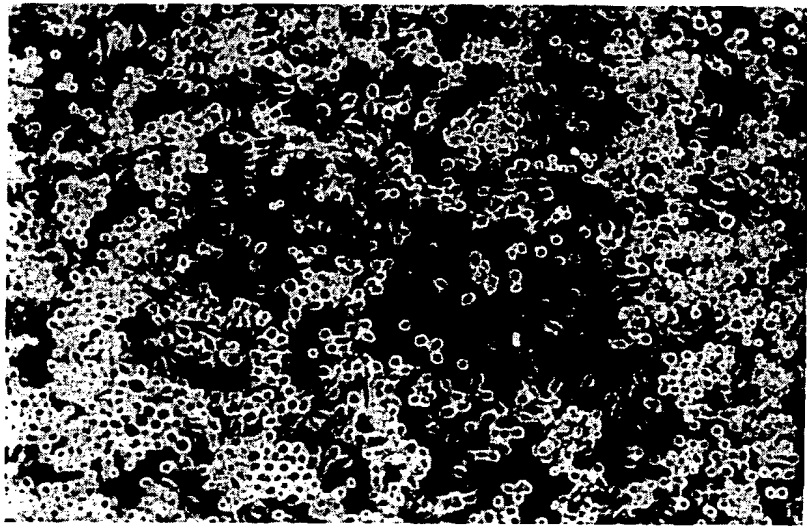


FIGURE 13

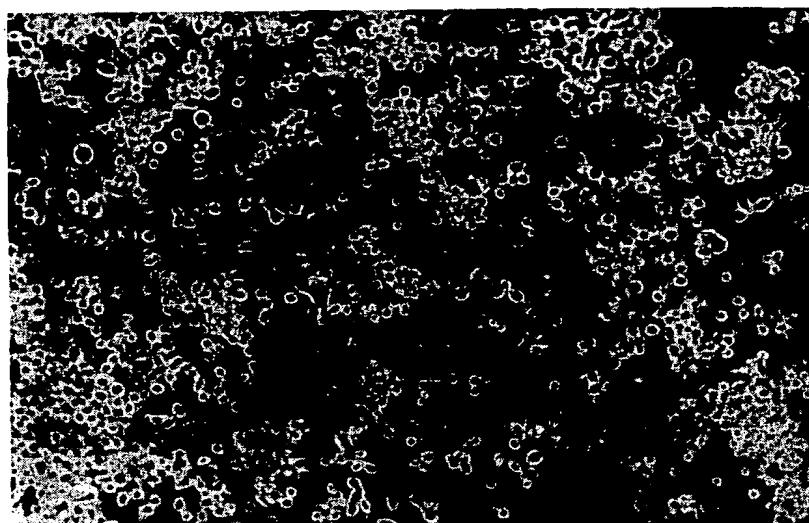


FIGURE 14

SM E M NP E+M+NP SM

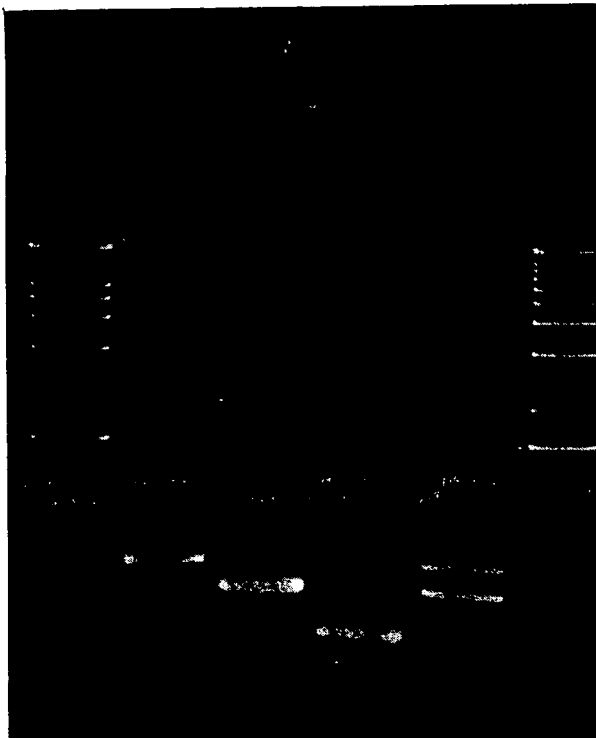


FIGURE 15

SM pVL1393 E M NP SM

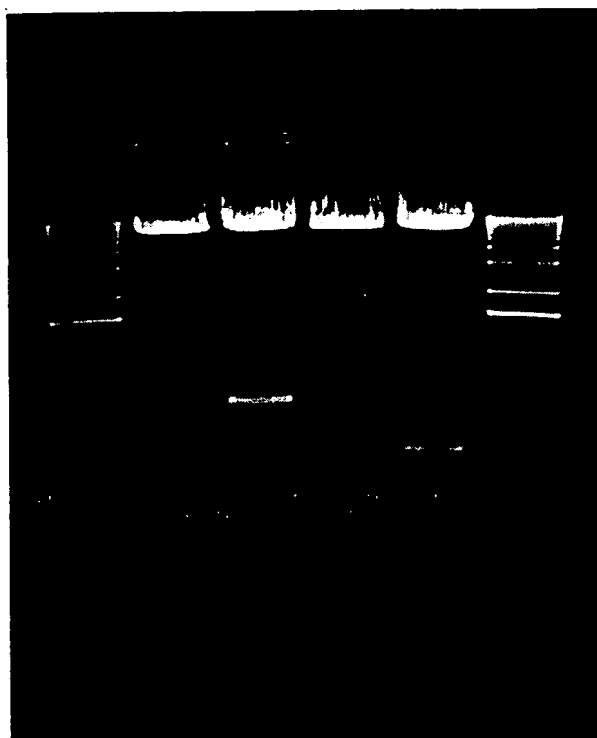


FIGURE 16

FIGURE 17

	ORF 6 start	
	+ 1>	
VR 2385	ATGAGTCTGTCCTTAGATGACTTTGTGCATGATAGCACGGCTCCACAAAGGTGCTTTGGCGTTTTCTATTACCTACACGCCAGTGATATATATGCCC	100
ISU-1894	. . . G C . . . T T	100
ISU-22	. . . G C . . . C T	100
ISU-79	. . . G T . . . T T . . . A A	100
ISU-55	. . . G C . . . T . . . CA T . . . C G T	100
ISU-3927	. . . G . . . C . . C . . T . CA . . . CCT . TC . CG . . . C . CG . GC . A . C . AGC . C . A . . TA . A . . . C . . .	97
LV	. . . G - A - G . C . . C . T . T . CA . C . . CCT . TC . CG . . . C . CG . GC . A . C . AGC . C . A . . TA . A . . . C . . .	
VR 2385	TAAAGGTGAGTCGGCGCCGACTGCTAGGGCTTCTGCACCTTTTGGTCTTCTGAATTGTCTTTACCTTCGGGTACATGACATTGGTGCACTTTTCAGAG	200
ISU-1894 A	200
ISU-22 A C	200
ISU-79 A A	200
ISU-55	. . . A . A A . T . T T . T G	200
ISU-3927	. . . A A . T . T T . T AT . . . T . . . ATC	199
LV	. T . . . TCA C . G . . GT . . A . CC . AA . A . T . . . C . T . C . T . A . . A . . AT . . T . . ATC	
VR 2385	TACAAATAAGGTCCGCGCTCACTATGGGAGCAGTAGTTGCACTCCTTTGGGGGGTGTACTCAGC--CATAGAAACCTGGAAATTCATCAGCTCCAGATGCC	298
ISU-1894	298
ISU-22 A	298
ISU-79	298
ISU-55	C . . . C C . . . T . C	298
ISU-3927	C . . . G A . T . CC . . G . T . T . C . -- CCT . C . T . . . TTA . . TT . C . ; GT . A . . G . T . . T . . . A	295
LV	C . C . CCGT . . . A . T . CC . . G . T . T . C . -- CCT . C . T . . . TTA . . TT . C . ; GT . A . . G . T . . T . . . A	
VR 2385	GTTTGTGCTTGCTAGGCGCGAAGTACATTCTGGCCCCCTGCCACCACGTTGAAAGTGCCGCGAGGCTTTCATCCGATTGCGGCAAATGATAACCAACGCATT	398
ISU-1894	398
ISU-22	398
ISU-79 T A	398
ISU-55 T G	398
ISU-3927	. A . . . T . GC . T . . GCCA T . . . A . . . T . . . TC . C . . T . A . CT . A . GTC . G . . GA . . A	395
LV	. A . . . T . GC . T . . GCCA T . . . A . . . T . . . TC . C . . T . A . CT . A . GTC . G . . GA . . A	
VR 2385	TGTCGTCCGGCGTCCCGGCTCCACTACGGTCAACGGCACATITGGTGCCCGGTTAAAAAGCCTCGTGTITGGGTGGCAGAAAAGCTGTTAAACAGGGAGTG	498
ISU-1894 G	498
ISU-22 T G	498
ISU-79 T G C	498
ISU-55 T G . G . . . A G	498
ISU-3927	C . CT . GA . AAA . . ACTA . AT . A . G . . . TC . A . A . A . AC . TCGG . . . C . . C . . A . CG . . . GA . . .	495
LV	C . CT . GA . AAA . . ACTA . AT . A . G . . . TC . A . A . A . AC . TCGG . . . C . . C . . A . CG . . . GA . . .	
	ORF 7 start + 1> *** ORF 6 stop	
VR 2385	GTAACCTTGTTTAAATAAGCCAATAAACACCGGCA-AGCAGCAGAAGAGAAAGAA-----GGGGGATGGCCAGCCAGTCAATCAGCTGTG	582
ISU-1894 C A	582
ISU-22 C A . T	582
ISU-79 C A	582
ISU-55 A A	582
ISU-3927 A A	582
LV	. T . . . C . C . G . . G . CGG . . A . A . -- G A . . . AAGTACAGCTCCGAT . . . A A . . .	591

VR 2385	CCAGATGCTGGGT--AA-GATCATCGCTCAACCAAAACAGTCCAGAGGCAAGGGACCGGAAAGAAAAATAAGAAGAAAAACCCGAGAAGCCCCATTTC	679
ISU-1894 G C	679
ISU-22 C G . . . T	679
ISU-79 C C . . . T	679
ISU-55 C C	679
ISU-3927	. A C . G . . . T	679
LV	. T GC . T . . A . AGT . C . G . -- G CCT . G C . . . -- GCC . A . . . G . T . . . A . . . T	679
VR 2385	CCTCTAGCGACTGAAGATGATGTCAGACATCACTTTACCCCTAGTGAGCGTCAATTGTGTCTGTCTGTCAATCCAGACCGCCTTTAATCAAGGCGCTGGGA	779
ISU-1894 C G	779
ISU-22 G A . T	779
ISU-79 C . . T . G . . . G A A	779
ISU-55 C . . C . . G T G	779
ISU-3927	. C . G . TG . . . CA . C . G . C . . C . C . AG . C . A . CTC . C . CT . CAA . G G . T . C . . . A . A .	779
LV	. C . G . TG . . . CA . C . G . C . . C . C . AG . C . A . CTC . C . CT . CAA . G G . T . C . . . A . A .	
VR 2385	CTTGCAACC-CTGTGAGATTACGGGAGGATAAGTTACACTGTGGAGTTTAGTTTGCCCTACGCATCATACTGTGCGCCTGATCCGCGTCAAGCATCACCC-	877
ISU-1894 A	877
ISU-22	877
ISU-79 T	877
ISU-55	. . . T G	877
ISU-3927	. C . T . T . . A G T G . . C . .	877
LV	. . . GT . G . T . . TCCAGC . . A . G . C . . TTCAG . T TGC . . GGTTGC . . . A T . . . G . TT . TA . T . G	878
	*** ORF 7 stop	
VR 2385	TCAG-CA-----TGA	886
ISU-1894	886
ISU-22	886
ISU-79	886
ISU-55	886
ISU-3927	886
LV	C . . T . . GGGTGCAAGT.A.	898

A

VR 2385 ORF6	MESSLDDFCHDSTAPQKVLLAFSITYTPVMYALKVSRGRLGLLHLLVFLNCAFTFGYMTFVHFQSTNKVALTMGAVVALLWGVSAIETWKFITSRCR	100
ISU-1894 ORF6	.G.....I.....	100
ISU-22 ORF6	.G.....I.....	100
ISU-55 ORF6	.G.....I.....	100
ISU-79 ORF6	.G.....Y.....I.....M.....	100
ISU-3927 ORF6	.G.....N.....I.....E.....R.....	100
LV ORF6	.G-G.....N.PI.A..LV.....I.....I.....S.....Y.....R.....L.....FT.S.....	99
PRRSV-10 ORF6	.G-G.....N.PI.A..LV.....I.....I.....S.....Y.....R.....L.....FT.S.....	99
LDV-C ORF2	.G-G.-E..DQTSWY.-IFI...L...IA..S...F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL...I..V..I..TLVKIVDWLVI...	96
LDV-P ORF2	.G-G.-E..DQTSWY.-I.I...L...IA..S...F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..T...SL...I..V..I..TLVKIVNWMVL...	96

VR 2385 ORF6	LCLLGRKYILAPAHVESAAGFHPAANDNH-----AFVVRRPGSTTVNGTLVPLKSLVLGGRKAVKQGVNVLVKY-AK	183
ISU-1894 ORF6	174
ISU-22 ORF6	174
ISU-55 ORF6	174
ISU-79 ORF6	174
ISU-3927 ORF6R.....K.....	174
LV ORF6	.C...R.....L.S.S.SG.R-----YA..K..L.S.....R.....KR...R.....-GR	173
PRRSV-10 ORF6	.C...R.....L.S.S.SG.R-----YA..K..L.S.....R.....KR...R.....-GR	173
LDV-C ORF2	.P...S.....PS..D-----TSDGRQSLTTSITT.....K...L...Q...DFQR.....K...SK.A...L..VS.	171
LDV-P ORF2	.F...S.....PS..D-----TSDGRQSLTTSITT.....K...L...Q...DFQR.....K...SK.A...L..VS.	171

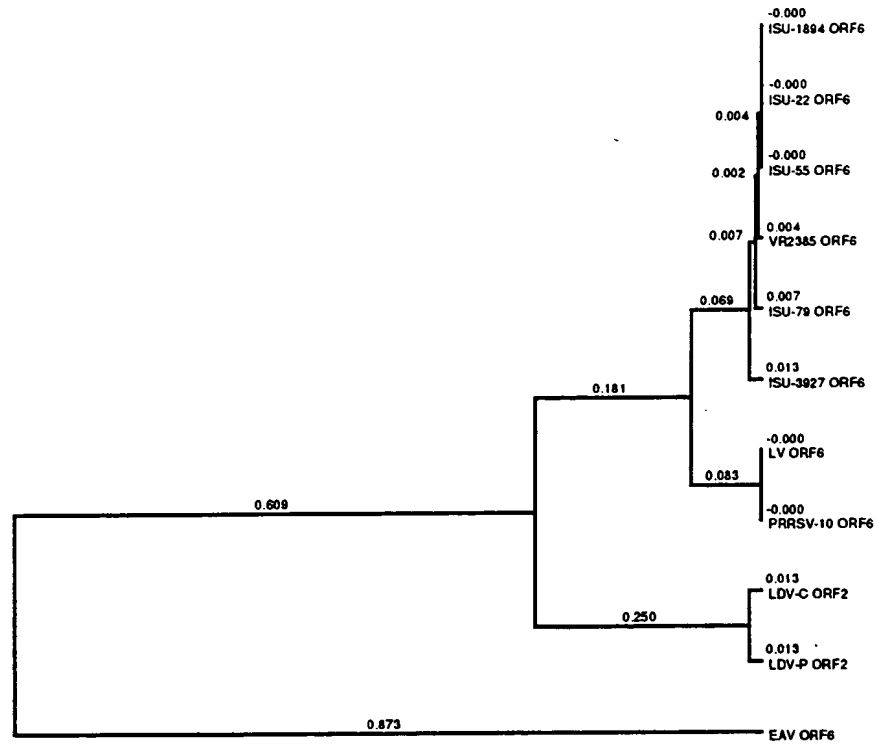
B

VR 2385 ORF7	MPNNTGKQQRKK-----GDGPVNQLCQMLGKI IAHQNSRGKGPCKKKNPEKPHFPLATEDDVRHHTPSEKQLCLSSIQTAFNQAGTCTLS	100
ISU-1894 ORF7	...N.....Q.....	93
ISU-22 ORF7	...N.....Q.....	93
ISU-79 ORF7	...N.....Q.....	93
ISU-3927 ORF7	...N.....K.....Q.....I..	93
ISU-55 ORF7	...N.....K.....Q.....SG.....	93
VR2332 ORF7	...N...TEE.....Q.....	93
LV ORF7	---A..N.SQ..KKSTAPM.N.....L..AM.KS.R---QPR.GQA...K.....A...I...L.QT..S...Q.....AS..	94
PRRSV-10 ORF7	---A..N.SQ..KKSTAPM.N.....L..AM.KS.R---QPR.GQA...K.....A...I...L.QT..S...Q.....PS..	94
LDV-C ORF1	.SQ.KK.GGQN-----AN-----N.LISALLRNAG.--N..K.Q.K.-Q.-L...M.GPS.L..VM..N.V.M.R..LV.L...G.Q...V	85
LDV-P ORF1	.SQ.KK.GGQN-----AN-----N.LINALLRNAG.--N..K.Q.K.-Q.-L...M.GPS.L..VM..N.V.M.R..LV.L...G.Q...V	85
EAV ORF7	.ASRRSRP.AASF-----RN.R--RRQPTSYNDLLRMFG-----MRVR.PPAQPTQAI.I.EPG.L..DLNQQ..ATLS.NV.RF.MI.H.SL.-A	83

VR 2385 ORF7	DSGRISYTFEFLPTHHTVRLIRVTASP----SA	134
ISU-1894 ORF7	123
ISU-22 ORF7	123
ISU-79 ORF7	123
ISU-3927 ORF7P.....	123
ISU-55 ORF7	123
VR2332 ORF7	123
LV ORF7	S..KV.FQ...M..VA.....STSASQGAS	128
PRRSV-10 ORF7	S..KV.FQ...M..VA.....STSASQGAS	128
LDV-C ORF1	...G.NF..S.M....A.....NAS.NS-----	115
LDV-P ORF1	...G.NF..S.M....A.....NAS.NS-----	115
EAV ORF7	.A.GLT...SW-V..KQIQ.KVAPP.G-----	110

FIGURE 18

A



B

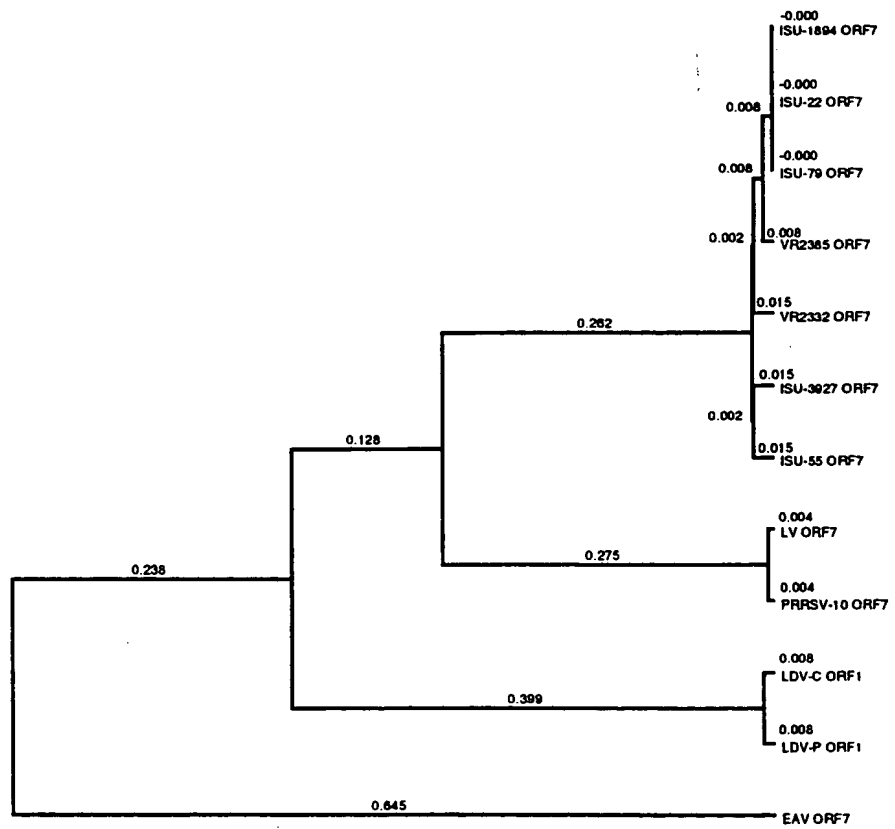


FIGURE 19

+ Start ORF2
 CCTGAATTGAGATGAAATGGGGTCTATGCAAAGCCTTTTGTGACAAAATTGGCCAACCTTTTGTGGATGCTTTCACGGAGTTCTTGGTGTCCATTGTTGAT 100
 ATCATTATATTTTGGCCATTTTGTGTTGGCTTCACCATCGCAGGTGGCTGGTGTCTTTTGCATCAGATTGGTTTGTCTCCGCGATACTCCTGTGGCGCC 200
 CTGCCATTCACTCTGAGCAATTACAGAAGATCCTATGAGGCCCTTCTCTCTCAGTGCAGGTGGACATTCCACCTGGGGAACTAAACATCCTTTGGGGA 300
 TGCCTTGGCACCATAGGTGTCAACCTGATTGATGAAAATGGTGTGCGCTCGAATGTACCGCATCATGGAAAAAGCAGGACAGGCTGCCTGGAACAGGT 400
 AGTGAGCGAGGCTACGCTGTCTCGCATTAGTAGTTTGGATGTGGTGGCTCATTTTCAGCATCTTGGCCGCAATTGAAGCCGAGACCTGTAAATATCTGGCC 500
 TCTCGGCTGCCCATGCTACACCACTGCGCATGACAGGTCAAAATGTAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTTGTCTTTTCCAACTCC 600
 + Start ORF3
 CTGGTTCCCGGCCAAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCTCTATATTTTCTCTGTTGCAGCTTCTTGTACTCTTTTGTGTTGT 700
 GCTGTGGTTGCGGGTTCCAATGCTACGTACTGTTTTGGTTTCGCTGGTTAGGGGCAATTTTCTTTTCGAACTACGGTGAATTACACGGTGTGCCCGC 800
 *** Stop ORF2 ↓
 CTTGCCCTACCCGGCAAGCAGCCGAGAGGCCCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATCGATGTGGGGAGGACGATCATGATGA 900
 ACTAGGGTTTGTGGTGCCTGTGGCTCTCCAGCGAAGGCCACTTGACCACTGCTTACGCCCTGGTTGGCGTCCCTGTCTTCAGCTATACGGCCCACTTC 1000
 CATCCCGAGATATTCGGGATAGGGAAATGTAGTCGAGTCTATGTTGACATCAAGCACCAATTTCATTTGCGCTGTTTCATGATGGGCAGAACACCACTTGC 1100
 + Start ORF4
 CCCACCATGACAACATTTTCAGCGTGTCTTACAGCTATTACCAGCATCAGGTGACGGGGCAATTGGTTTCACCTAGAAATGGGTGCGTCCCTTCTTTTC 1200
 CTCCTGGTTGGTTTAAATGTCTCTTGGTTTCTCAGGCGTTGCGCTGCAAGCCATGTTTCAGTTGAGTCTTTTCAGACATCAAGACCAACACCAACCGCAG 1300
 CGGCAGGCTTTGCTGTCTCTCAAGACATCAGTTGCCCTTAGGCATCGCAACTCGGCCTCTGAGGCGATTGCAAAAGTCCCTCAGTGGCCGACGGCGATAGG 1400
 *** Stop ORF3
 GACACCCGTGTATATCACTGTCAAGCCAATGTTACCGATGAGAATTATTTGCATTCTCTGATCTTCTCATGCTTTCTTCTTGGCTTTTCTATGCTTCT 1500
 GAGATGAGTGAAAAGGGATTTAAGGTGGTATTTGGCAATGTGTCAAGCATCGTGGCAGTGTGCGTCAACTTCACCACTTACGTCCAACATGTCAAGGAAT 1600
 TTACCCAACGTTCTTGGTAGTTGACCATGTGCGGCTGCTCCATTTTCATGACGCCGAGACCATGAGGTGGGCAACTGTTTTCAGCTGTCTTTTACCAT 1700
 ***Stop ORF4 +Start ORF5
 TCTGTTGGCAATTTGAATGTTTAAAGTATGTTGGGGAAAATGCTTGTACCGCGGGCTGTTGCTGCAAAATGCTTTTTTATGGTGTATCGTGGCGTCTGTT 1799

FIGURE 20

A

Consensus	M.WG.C..K.....L...W.....L..SL...P..CL.SPSQ.G.WSF.S.WFAPR.SVRALPFTL.NYRRSYE...L..C..D.P....KH	100
LV ORF2.	.Q..H.GV.SASCSWTPS.SSLLV.LI-----PF.....Y..G...D.Y...F.E.....F.....P.....GL.PN.RP.V.QFAV..	90
VR2385 ORF2.	.K..L-----AFLTK.AN-FL.MLSRSSWCP.LI..YFW.F..A...V.W...A.D....Y.....S.....AF.SQ.QV.I.TWGT..	93
Consensus	PLGM.WH..VS.LIDEMVSRR.Y..ME..GQAANKQVV.EATL...S.LD.V.HFOHLAA.EA..C..L.SRL.ML..L.....NV...YN.TL..V...	200
LV ORF2.	...F..MR..H.....I.QT..HS.....G....TKL.G..I.T.....V..DS.RF.S...V..KN.AV--G..SLQ..T..DR.ELI	188
VR2385 ORF2.	...L..HK..T.....M.RI..KA.....S....SRI.S..V.A.....I..ET.KY.A...P..HH.RMTGS..TIV..S..NQ.FAV	193
Consensus	FPTPG.RPKL.DP.QWLI.VH.SIFSSVA.S.TLF.VLWLR.P.LR.VFGF.W..A.....	264
LV ORF2.	...T...T.R.....S..A.....S.V...I...I.A..Y...H.PT---THHSS	249
VR2385 ORF2.	...S...H..Q...A..S.....A.C...V...V.M..T...R.LG.IFLNSR-	257

B

Consensus	MA..C.....FLC....Y....A....S..T.CFWPPL..GN.SFELT.NYT.C.PC.T.QAA....EPGR..WC.IGHDRC.E.DHDEL....PSG...	100
LV ORF3.	..HQ.ARFHF...GFIC.LVHS.LASN.SS.L.....AH..T.....I...I.M..S.S...RQRL...NM..K.....E.R.....LMSI...YDN	100
VR2385 ORF3.	..NS.TFLYI...CSFL.SPCC.VVAG.NA.Y.....VR..F.....V..V.P..L.R...AEAY....SL..R.....G.D....GFVV...LSS	100
Consensus	...L...YAWLA.LSPSY.AQFHPE.FGIGNVSRV.VD..HOFICA.HDG.N.T.....NISA....YY.HQ.DGGNWFHLEW.RP.FSSWLVLN.SWFL	200
LV ORF3.	L-K.EGY....F....A.....L.....F..KR.....E..H.S.VSTGH....LYAA..H..I.....L..L.....I.....	199
VR2385 ORF3.	BGH.TSA.....S.....T.....I.....Y..IK.....V..Q.T.LPHHD...VLQT..Q..V.....V..F.....V....	200
Consensus	RRSP.S.VS.R..Q..RPT.P.....S..TS....L.....R.F.....K.S.....	266
LV ORF3.	...V.P..R..IY..IL...R.RLPVSW.FR...IVSD.TGSQQRK.K.PSESRRNVV.P.VLPSTSR	265
VR2385 ORF3.	...A.H..V.VF.TS...P.QRQALL.SK..V--A.GIATRPL.R.A-----LSAARR-	255

C

Consensus	M.A..LF.L.G....VS.APACKPCFS..LSDI.TMTTAAAGF.VLQDI.C.R.....A.E.I...K..QCR.A.GTP.YIT.TANVTDE.YL...DL	100
LV ORF4.	.A.AT..F.A.AQHIM..E.....TH...E.....M.....N.P.PHGUSA.Q.K.SFG.SS...E.V...Q...I.....S..YNA..	100
VR2385 ORF4.	.G.SL..L.V.FKCLL..Q.....SS....K.....A.....S.L.HR--NS.S.A.R--VP...T.I...V...V.....N..HSS..	96
Consensus	LMLS.CLFYASEMSEKGFKV.FGNVSG.V..CVNFT.YV.HV...TQ...V...RLLHF.TP..MRWAT..ACLF.IILLAI.	184
LV ORF4.	...A.....I.....V.SA....D..A..TOH..QHHL.IDHI....L..SA.....TI....A.....	183
VR2385 ORF4.	...S.....V.....I.AV....S..Q..KEF..RSLV.DH-V.....M..ET....VL....T.....	179

FIGURE 22

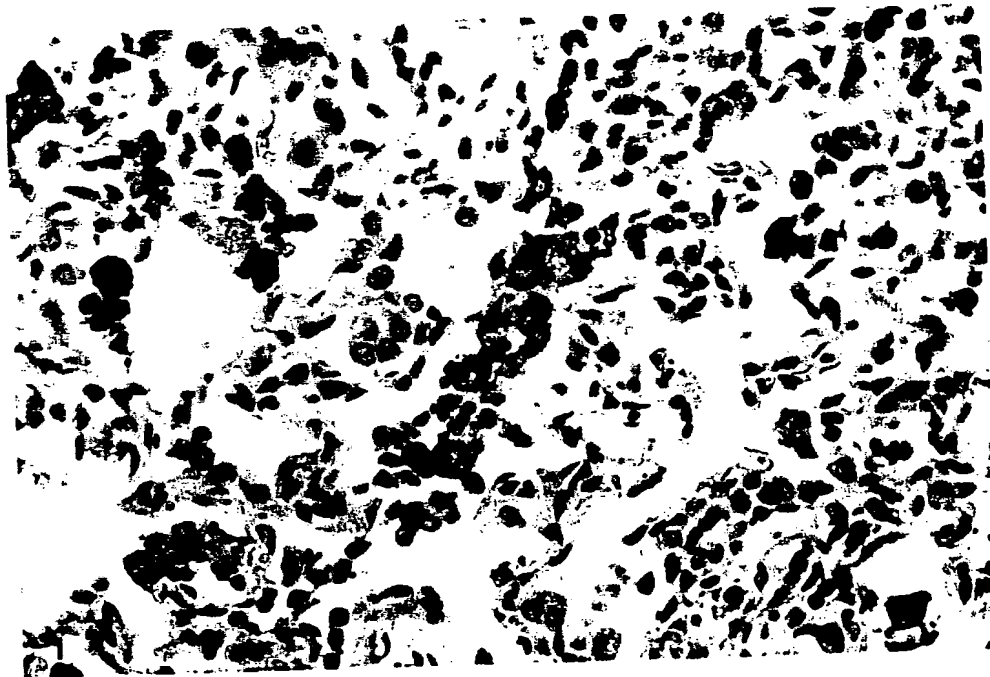


FIGURE 23

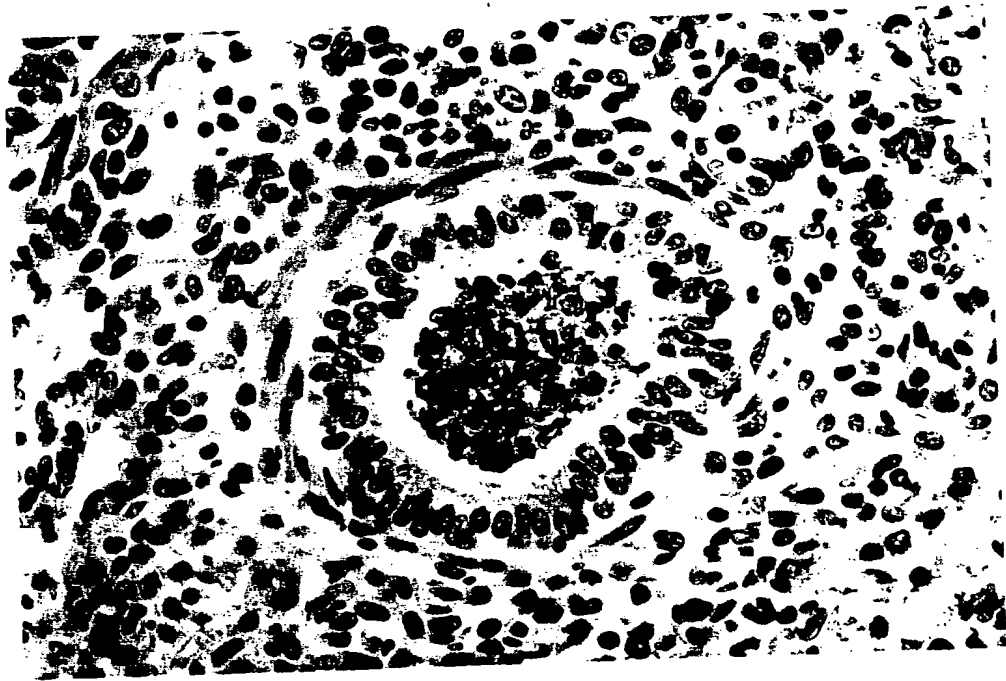


FIGURE 24

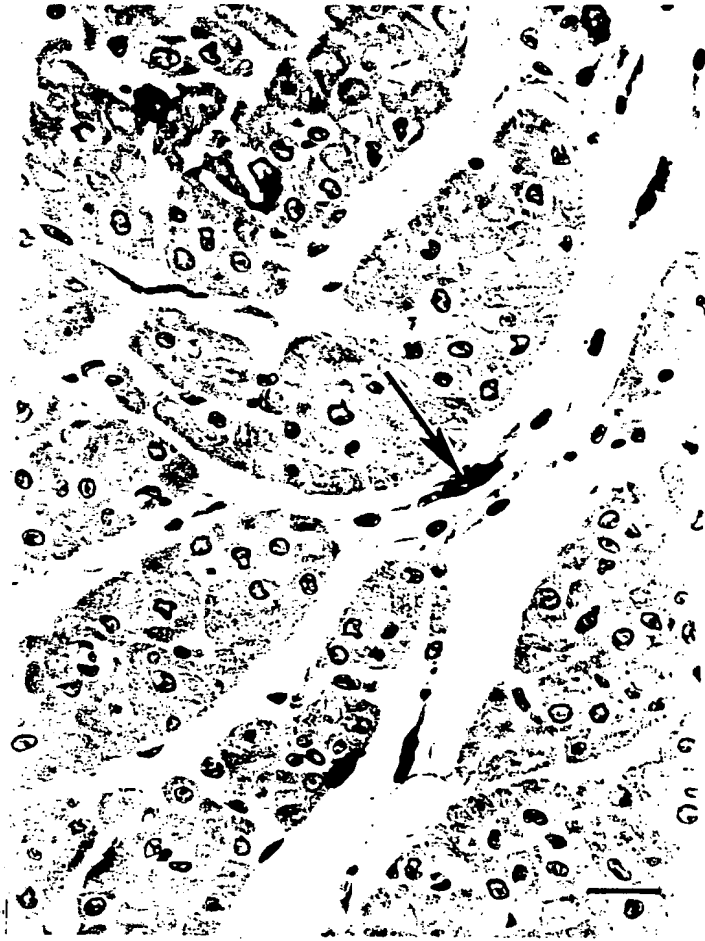


FIGURE 25

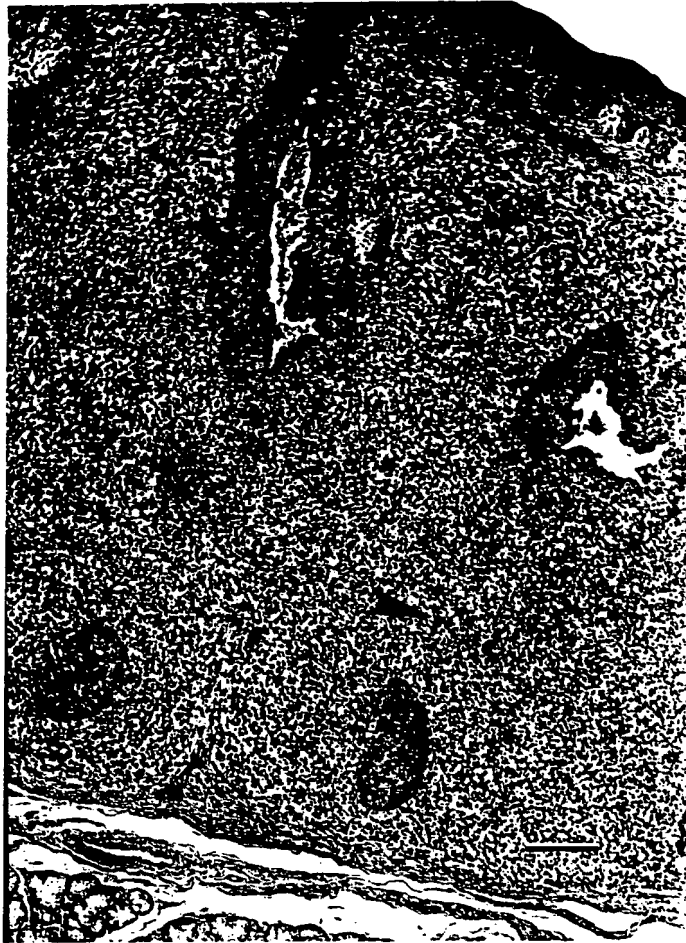


FIGURE 26

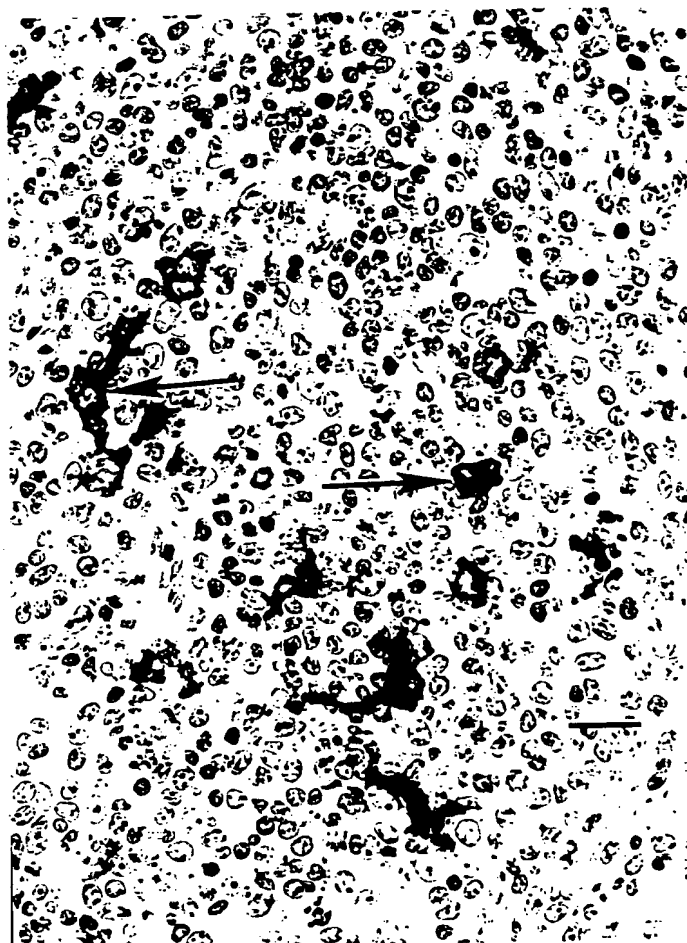


FIGURE 27



FIGURE 28

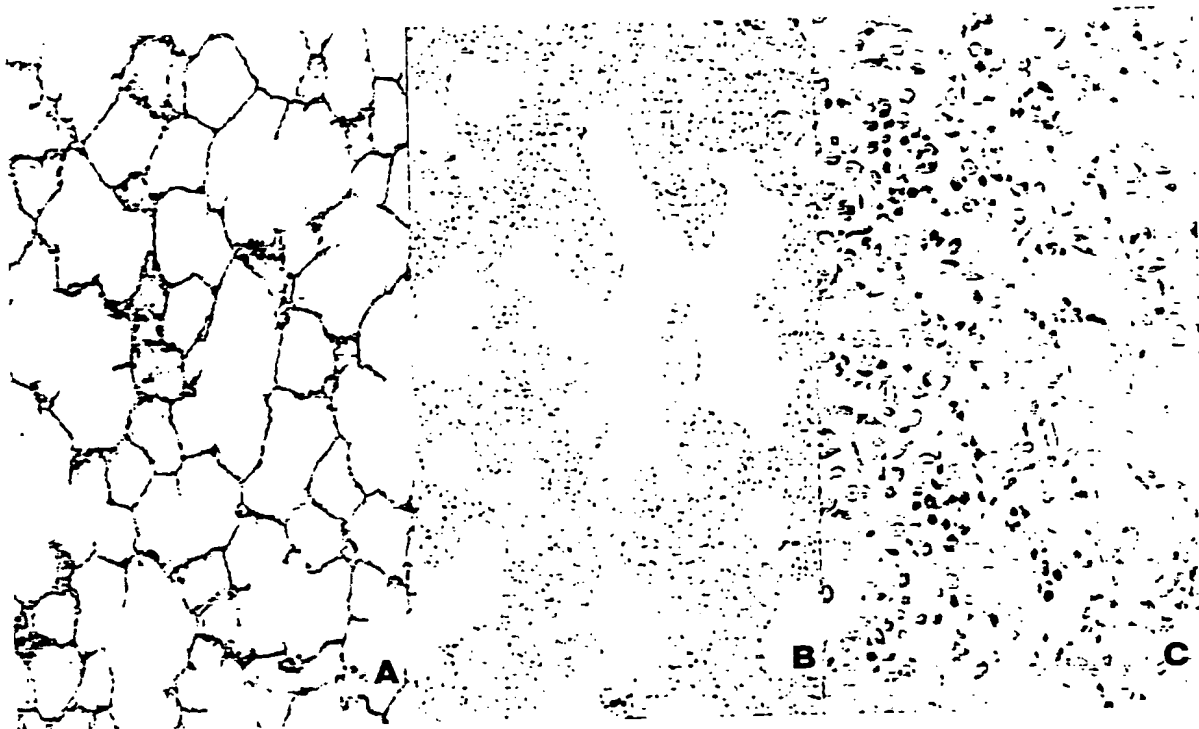
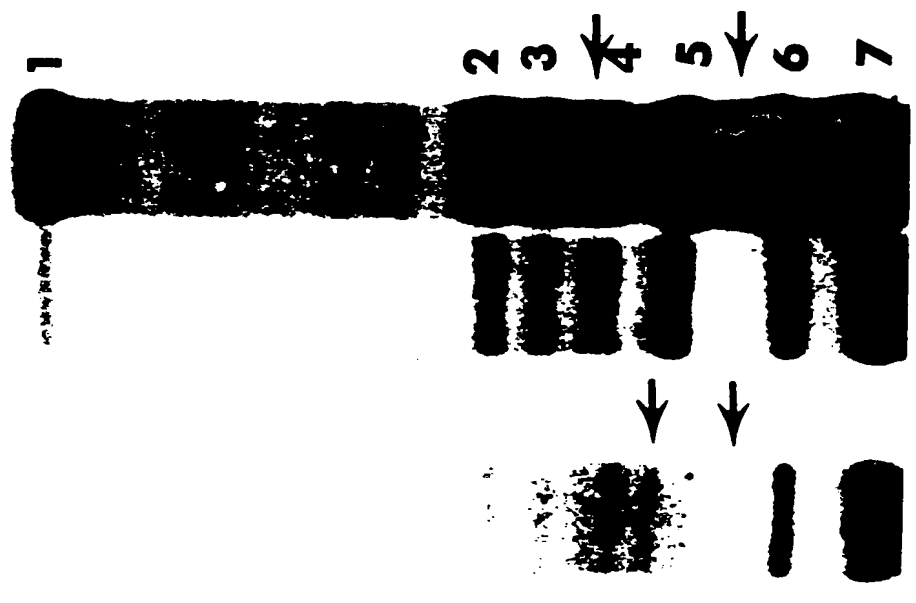


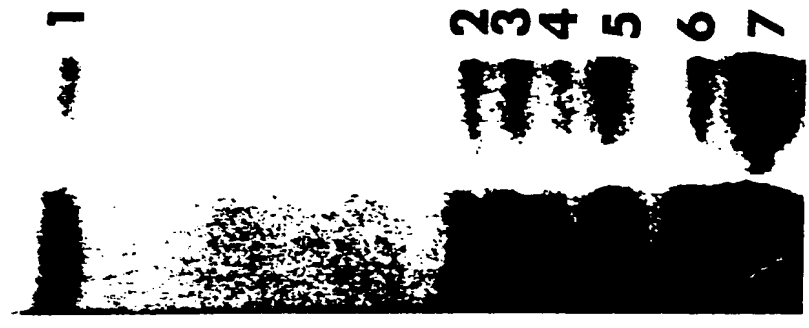
FIGURE 29

1894 3927

22 55 79



A



B

FIGURE 30